STIC Search Report
Biotech-Chem Library

USPTO

To: Susan Ungar
Location: CM1-8B05
Art Unit: 1642
Wednesday, June 04, 2003

82-12

Case Serial Number: 09/125005

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

Seq. ID 6 (09/125005) v. P04637 (SwissProt_40)

sira
Search and Information
Resources Administration

95795

From:	Hart, Edward
Sent:	Wednesday, June 04, 2003 11:40 AM
T :	Shears, Beverly
Subject:	FW: 09/125,005

Here is a rush search that I received.

Edward

-----Original Message-----
From:	Chan, Christina
Sent:	Tuesday, June 03, 2003 8:46 AM
T :	Ungar, Susan
Cc:	Hart, Edward
Subject:	RE: 09/125,005

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----
From: Ungar, Susan
Sent: Tuesday, June 03, 2003 8:30 AM
To: Chan, Christina
Cc: Hart, Edward
Subject: 09/125,005

Hi

I'm working on this case now, its due this biweek.

I need a very very rush comparison of SEQ ID NO:6, human p73, with PO4637, human p53 which is a hit that was picked up in the sequence search of November 7, 2002 on SwissProt_40. It was number 24 on the list but was not printed out because I did not request a printout beyond the normally sent number.

I need this one very fast, if its quicker to do the regular search and leave out the interference search thats fine, but I would need to have hits 1-45 printed out.

Ed Hart has agreed to submit this polypeptide search for me, please send authorization directly to him.

Thanks
Susan Ungar
1642
703-305-2181
CM1-8B05

SEARCH REQUEST FORM

Requestor's
Name: _____   Serial
Number: _____

Date: _____   Phone: _____   Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 06-04-03
Searcher: Beverly C4994
Terminal time: 30
Elapsed time: _____
CPU time: _____
Total time: 42
Number of Searches: _____
Number of Databases: 2

Search Site
_____ STIC
_____ CM-1
_____ Pre-S

Type of Search
_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors ✓
_____ IG Suite
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
___✓___ Other GCG

Wed Jun 4 14:33:08 2003

us125006_6xp04637.rec

```
>O<
OI IO   IntelliGenetics
>O<
```

GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Wed 4 Jun 103 14:29:54 PDT

Solution Parameters:

```
Amino Alphabet        = Identity
Output line length    = 80
Compress              = Off
Histogram             = Off
Randomization         = Off

AMINO-Res-length      = 2
DELetion-weight       = 5.00
LEngth-factor         = 0
Matching-weight       = 1.00
NUCLEIC-Res-length    = 4
SPread-factor         = 50
```

Clustered order of selected sequences:

```
1. p04637            (1-393)
4. US-09-125-005-6   (1-636)
```

Region Alignment: (listed in Clustered order)

```
p04637        1   meePqsdpsvEpplSqetfsdlwkllP       eNNvlsplpsqaMD dlmlspddie
                                |  |||| |            |  ||            ||
US-09-125-    1   maqstatsPdqgttfEhlwSslepdstyfdLPqssrgNnevvggtdssMDvfhlegmttsv
consensus         maqst--P------E---S---------LPqssr-NN--------MDv---------

p04637       52   qwftedgpdeaprmpeAA  pPvaPapAA   PT    paqapapapswplsssvPSqktYq
                                  ||      |  |        |                 ||    |
US-09-125-   62   maqfnllsstmdqmssrAAsasPytPehAAsvPThspyaqpsstfdtmspapviPSntdYp
consensus         ----------------AAsa-P--P--AAsvPThspy-------------PS---Y-

p04637      105   GsygFrlgFlhSgTAKSvTcrYSPaLnKmfCQlAKTCPvQlwVdstPPPGTrvRAMalYKq
                   |  | | | | | |||| | | |||| | |||| |||||| | | ||||||| ||| |||
US-09-125-  123   GphhFevtFqqSsTAKSaTwTySPlL&KklyCQiAKTCPiQikVstpPPPGTaiRAMpvYKk
consensus         G--F---F--S-TAKS-T-TYSP-L-K--CQ-AKTCP-Q--V---PPPGT--RAM--YK--

p04637      166   sqHmTeVvrCPhHE   RcsdsdglAPpqHLIRVEGNlrveYlDDrnTfRhSVVVPYEPPe
                   | | | ||| ||       | |||  |||||||||   | ||| | | |||||||||||
US-09-125-  184   aeHvTdVvKRCPnHElgRdfneqqsAPasHLIRVEGNnlsqYvDDpvTgRqSVVVPYEPPq
consensus         --H-T-VV-RCP-HElgR------AP--HLIRVEGN---Y-DD--T-R-SVVVPYEPP-

p04637      225   VGsdcTTIhYNyMCNSSCmGGMNRRPILtIITLEdssGnlLGRnSFEvRvCACPGRDR  r
                  || || |||| |||||| |||||||||| |||||   |  ||| ||| | |||||||| |
US-09-125-  245   VGtefTTIlYNfMCNSSCvGGMNRRPILiIITLEmrdGqvLGRrSFEgRiCACPGRDRkad
consensus         VG---TTI-YN-MCNSSC-GGMNRRPIL-IITLE--G--LGR-SFE-R-CACPGRDRka-

p04637      284   teeenlrkkgephhelppgstKRA
                                       |||
US-09-125-  306   edhyreqqalnessakngaasKRAfkgsppavpalgagvkkrrhgdedtyylqvrgrenfe
consensus         ---------------------KRAfkgsppavpalgagvkkrrhgdedtyylqvrgrenfe

p04637      308   lpnntsssPQP
                           |||
US-09-125-  367   ilmklkeslelmelvPQPlvdsyrqqqllqrpshlqppsygpvlspmnkvhggmnklpsv
consensus         ilmklke-------PQPlvdsyrqqqllqrpshlqppsygpvlspmnkvhggmnklpsv

p04637      319
US-09-125-  428   nqlvgqpphssaatpnlgpvgpmlnnhghavpangemsssshsaqsmvsgshctpppyh
consensus         nqlvgqpphssaatpnlgpvgpmlnnhghavpangemsssshsaqsmvsgshctppppyh

p04637      319   kkKPldgEYFT  lqirgrerfemfRlneAL         eLK
                    | | |||||    ||||                      ||
US-09-125-  489   adpslvsfltglgcPnciEYFTsgglqslyhlqnltiEdglALkipeqyrmtiwrglqdLk
consensus         adpslvsfltg--p--EYFTsq-------E---ALkipeqyrmtiwrglq-LK

p04637      352   dAQ         AqkepGGSrahsshlskkgqtsRH  kklmfkteGPDsd
                   ||              |||                 ||          |||
US-09-125-  550   qghdystAQqllrssnaAtisiGGSgelqrqrvmeavhfrvRHtitipnrgggggGPDewa
consensus         qghdys-AQqllrssnaA---GGS-------RHtitl-------GPD-a

p04637      394
US-09-125-  611   dfgfdlpdckarkqpikeefteaeih
consensus         dfgfdlpdckarkqpikeefteaeih
```

Alignment score = -1057.00

Scoring matrix:

```
              1    4

        1               -1066
        1
        4
```